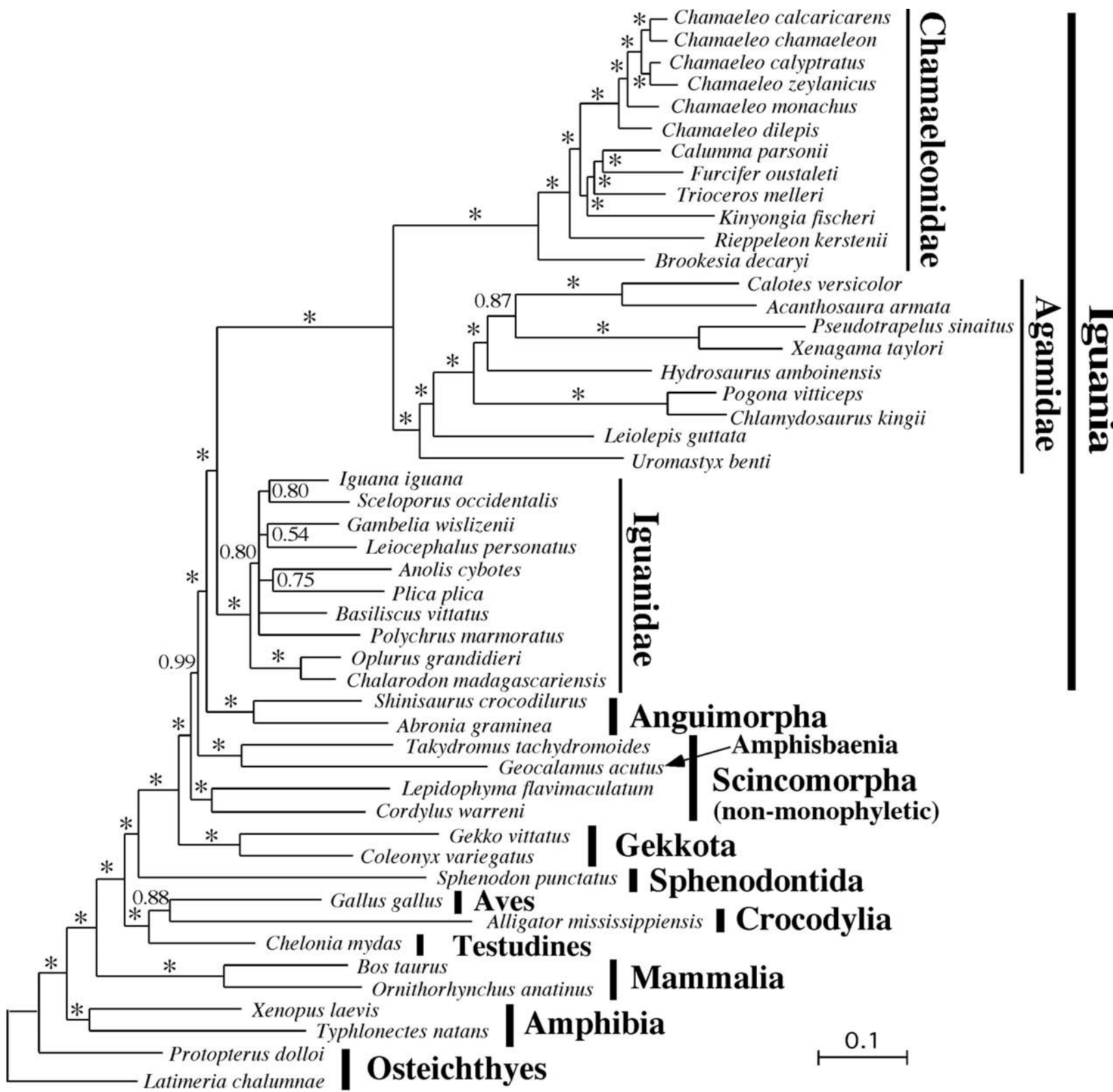




A Bayesian tree reconstructed using mitogenomic nucleotide sequences by including the tuatara and gap-containing sites (49 taxa, 9689 sites). Values shown are the Bayesian posterior probabilities and an asterisk stands for 1.00. See table 1 and Additional File 3 for accession numbers of mitogenomic data for individual taxa.